

[illegible]

Fig. 2

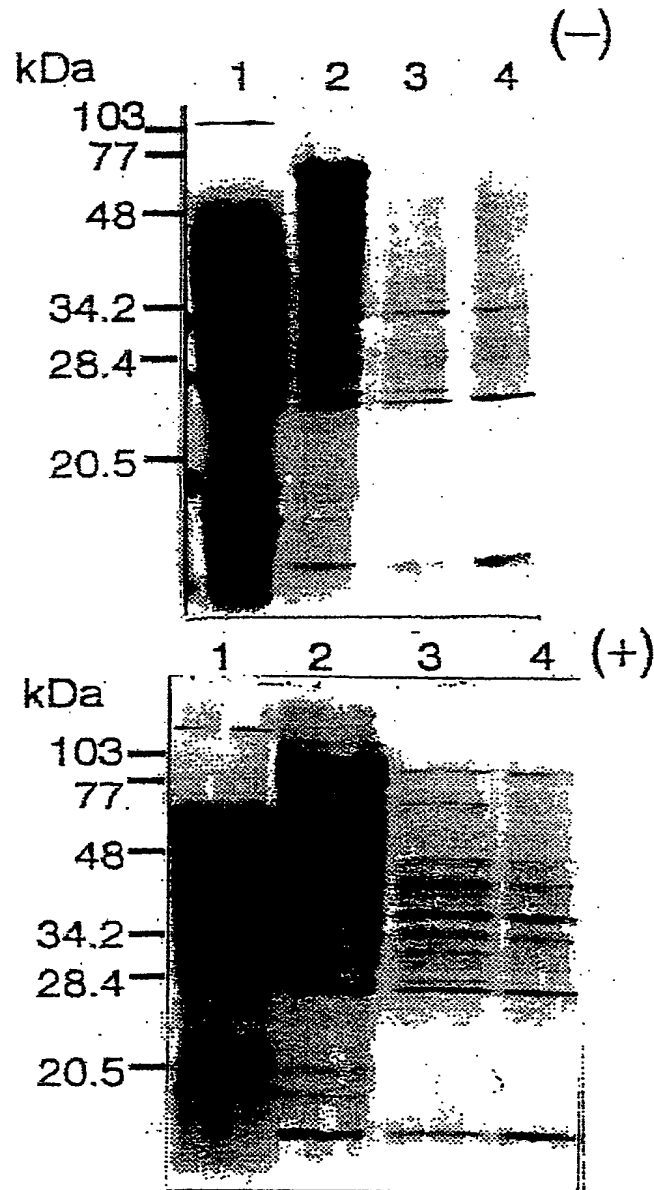
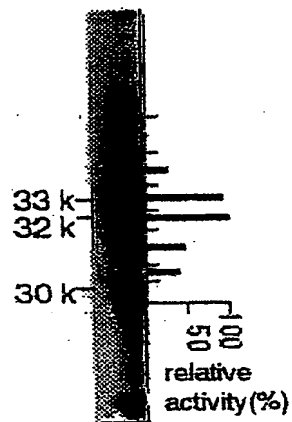


Fig. 3



09674337.072601

Fig. 4

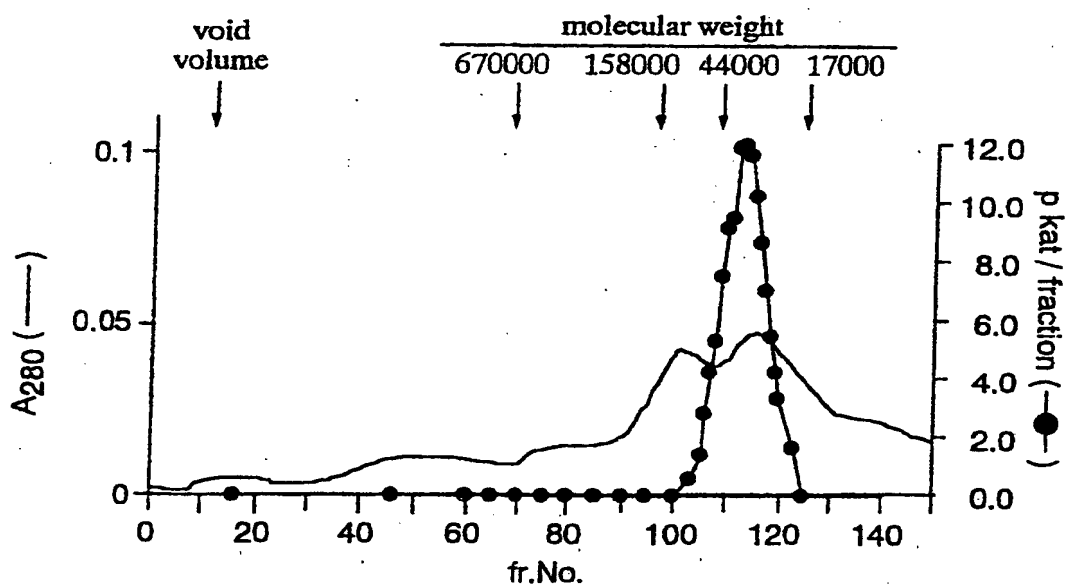


Fig. 5

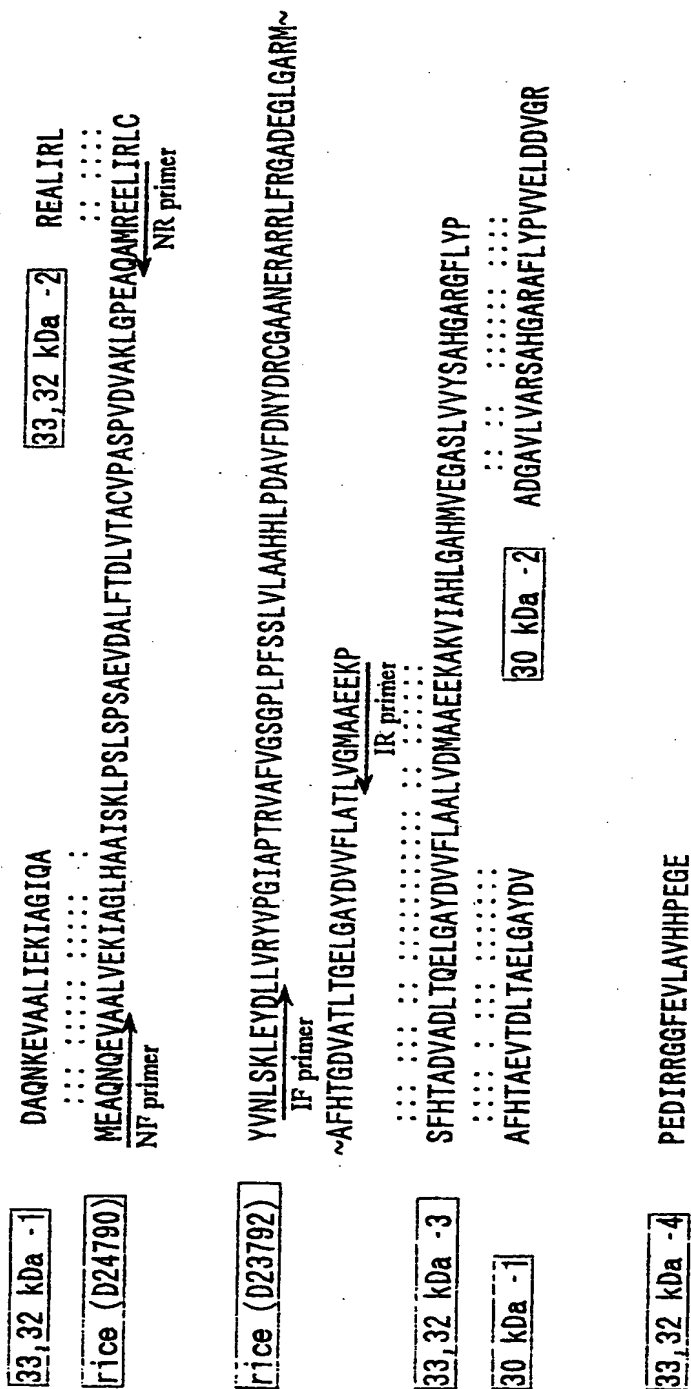


Fig. 6

	GCG	TTC	AGA	GGC	TTC	CAG	AGT	TCT	TCC	GGT	CAC	CAA	GAA	GCA	TTT	GAT	CAT	AAC	54
	ATG	GAT	GCC	CAG	AAC	AAG	GAG	GTC	GCT	GCT	CTG	ATC	GAG	AAG	ATC	GCC	GGT	ATC	108
19	M	D	A	Q	N	K	E	V	A	A	L	I	E	K	I	A	G	I	
	CAG	GCC	GCC	ATC	GCC	GAG	CTG	CCG	TCG	CTG	AGC	CCG	TCC	CCC	GAG	GTC	GAC	AGG	162
37	Q	A	A	I	A	E	L	P	S	L	S	P	S	P	E	V	D	R	
	CTC	TTC	ACC	GAC	CTC	GTC	ACG	GCC	TGC	GTC	CCG	CCG	AGC	CCC	GTC	GAC	GTG	ACG	216
55	L	F	T	D	L	V	T	A	C	V	P	P	S	P	V	D	V	T	
	AAG	CTC	AGC	CCG	GAG	CAC	CAG	AGG	ATG	CGG	GAG	GCT	CTC	ATC	CGC	TTG	TGC	TCC	270
73	K	L	S	P	E	H	Q	R	M	R	E	A	L	I	R	L	C	S	
	GCC	GCC	GAG	GGG	AAG	CTC	GAG	GCG	CAC	TAC	GCC	GAC	CTG	CTC	GCC	ACC	TTC	GAC	324
91	A	A	E	G	K	L	E	A	H	Y	A	D	L	L	A	T	F	D	
	AAC	CCG	CTC	GAC	CAC	CTC	GGC	CTC	TTC	CCG	TAC	TAC	AGC	AAC	TAC	GTC	AAC	CTC	378
109	N	P	L	D	H	L	G	L	F	P	Y	Y	S	N	Y	V	N	L	
	AGC	AGG	CTG	GAG	TAC	GAG	CTC	CTG	GCG	GCG	CAC	GTG	CCG	GGC	ATC	GCG	CCG	GCG	432
127	S	R	L	E	Y	E	L	L	A	R	H	V	P	G	I	A	P	A	
	GCG	GTC	GCC	TTC	GTC	GGC	TCC	GGC	CCG	CTG	CCG	TTC	AGC	TCG	CTC	GTC	CTC	GCC	486
145	R	V	A	F	V	G	S	G	P	L	P	F	S	S	L	V	L	A	
	GCG	CAC	CAC	CTG	CCC	GAG	ACC	CAG	TTC	GAC	AAC	TAC	GAC	CTG	TGC	GGC	GCG	GCC	540
163	A	H	H	L	P	E	T	Q	F	D	N	Y	D	L	C	G	A	A	
	AAC	GAG	GCG	GCC	AGG	AAG	CTG	TTC	GGC	GCG	ACG	GCG	GAC	GGC	GTC	GGC	GCG	CGT	594
181	N	E	R	A	R	K	L	F	G	A	T	A	D	G	V	G	A	R	
	ATG	TCG	TTC	CAC	ACG	GCG	GAC	GTC	GCC	GAC	CTC	ACC	CAG	GAG	CTC	GGC	GCC	TAC	648
199	M	S	F	H	T	A	D	V	A	D	L	T	Q	E	L	G	A	Y	
	GAC	GTG	GTC	TTC	CTC	GCC	GCG	CTC	GTC	GGC	ATG	GCA	GCC	GAG	GAG	AAG	GCC	AAG	702
217	D	V	V	F	L	A	A	L	V	G	M	A	A	E	E	K	A	K	
	GTG	ATT	GCC	CAC	CTG	GGC	GCG	CAC	ATG	GTG	GAG	GGG	GCG	TCC	CTG	GTC	GTG	CGG	756
235	V	I	A	H	L	G	A	H	M	V	E	G	A	S	L	V	V	R	
	AGC	GCA	CCG	CCC	GCG	GGC	TTT	CTT	TAC	CCC	ATT	GTC	GAC	CCG	GAG	GAC	ATC	AGG	810
253	S	A	R	P	R	G	F	L	Y	P	I	V	D	P	E	D	I	R	
	CGG	GGT	GGG	TTC	GAG	GTG	CTG	GCC	GTG	CAC	CAC	CCG	GAA	GGT	GAG	GTG	ATC	AAC	864
271	R	G	G	F	E	V	L	A	V	H	H	P	E	G	E	V	I	N	
	TCT	GTC	ATC	GTC	GCC	CGT	AAG	GCC	GTC	GAA	GCG	CAG	CTC	AGT	GGG	CCG	CAG	AAC	918
289	S	V	I	V	A	R	K	A	V	E	A	Q	L	S	G	P	Q	N	
	GGA	GAC	GCG	CAC	GCA	CCG	GGC	GCG	GTG	CCG	TTG	GTC	AGC	CCG	CCA	TGC	AAC	TTC	972
307	G	D	A	H	A	R	G	A	V	P	L	V	S	P	P	C	N	F	
	TCC	ACC	AAG	ATG	GAG	GCG	AGC	GCG	CTT	GAG	AAG	AGC	GAG	GAG	CTG	ACC	GCC	AAA	1026
325	S	T	K	M	E	A	S	A	L	E	K	S	E	E	L	T	A	K	
	GAG	CTG	GCC	TTT	TGA	TTG	AAG	AGT	GCG	CGT	GGT	CAT	TCT	GTC	GCC	TGC	GAT	CGT	1080
	E	L	A	F	*														
	GET	AAC	TTT	CCT	ACT	CGT	GTG	TGT	TTT	GAT	GTT	TGT	GCC	TGT	AAG	AGT	TAT	GCT	1134
	TCC	GGC	CTT	GTG	CTG	TTA	ATT	TAC	ACG	CGT	TAC	ATG	TAG	TAC	TTG	TAT	TTA	TAC	1188
	CTG	GAA	TAA	CGG	TAT	GTA	ACA	TAA	ATA	TTA	GTG	GGA	TTT	GAA	GTG	TAA	TGC	TAA	1242
	ATA	ATA	AGA	AAA	CTT	GAT	GCA	GAC	ATT	CAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AA	

HvNAS4 MDGQSE--EVDALVQKITGLHAAIAKLPSLSPSPDVALFTDLVTACVPPSPVDVTKLAP
 HvNAS7 MDAQSK--EVDALVQKITGLHAAIAKLPSLSPSPDVALFTDLVTACVPPSPVDVTKLAP
 HvNAS6 MDAQNK--EVDALVQKITGLHAAIAKLPSLSPSPDVALFTDLVTACVPPSPVDVTKLGS
 HvNAS2 MAAQNN-QEVDALVEKITGLHAAIAKLPSLSPSPDVALFTELVTACVPPSPVDVTKLGP
 HvNAS3 MAAQNNNKDVAALVEKITGLHAAIAKLPSLSPSPDVALFTELVTACVPPSPVDVTKLGP
 HvNAS1 MDAQNK--EVAALIEKIAGIAQAIAELPSLSPSPEVDRLFTDLVTACVPPSPVDVTKLSP
 HvNAS5 MEAENG--EVAALVEKITGLHAAISKLPALSPSPQVDALFTELVAACVPSSPDVTKLGP
 * ** ** * *** ** ***** ** *** ** **** *****

 HvNAS4 EAQAMREGLIRLCSEAEGKLEAHYSMDLAADFNDPLDHLGVFPYYSNYINLSKLEYELLAR
 HvNAS7 EAQAMREGLIRLCSEAEGKLEAHYSMDLAADFNDPLDHLGVFPYYSNYINLSKLEYELLAR
 HvNAS6 EAQEMREGLIRLCSEAEGKLEAHYSMDLAADFNDPLDHLGMFPYYSNYINLSKLEYELLAR
 HvNAS2 EAQEMREGLIRLCSEAEGKLEAHYSMDLAADFNDPLDHLGMFPYYSNYINLSKLEYELLAR
 HvNAS3 EAQEMREGLIRLCSEAEGKLEAHYSMDLAADFNDPLDHLGIFPYYSNYINLSKLEYELLAR
 HvNAS1 EHQRREALIRLCSAAEGKLEAHYADL LATFDNPLDHLGLFPYYSNYVNL SRLEYELLAR
 HvNAS5 EAQEMRQDLIRLCSAAEGLEAHYSMDLTALDSPLDHLGRFPYFDNYVNL SKLEHDLLAG
 * * ** ***** ** ***** * * * ***** ** ** *** ** ***

 HvNAS4 YVPGHRPARVAFIGSGPLPFSSYVLAARHLPTDVFNDYDLCSAANDRATRLFRADKD-V
 HvNAS7 YVPGGIAPARVAFIGSGPLPFSSYVLAARHLPTDVFNDYVVPVRAANDRATRLFRADKD-V
 HvNAS6 YVPGGIAPARVAFIGSGPLPFSSYVLAARHLPTDVFNDYDLCSAANDRASKLFRADKD-V
 HvNAS2 YVPGGYRPARVAFIGSGPLPFSSFVLAARHLPTDVFNDYDLCSAANDRASKLFRADRD-V
 HvNAS3 YVRR-HRPARVAFIGSGPLPFSSFVLAARHLPTDVFNDYDLCSAANDRASKLFRADTD-V
 HvNAS1 HVPG-IAPARVAFVSGSGPLPFSSVLAAHILPETQFDNYDLCSAANERARKLFGATADGV
 HvNAS5 HVAA--PARVAFIGSGPLPFSSFLATYHLPDTRFDNYDRCSVANGRAMKLVGAADGV
 * *** ***** ** *** **** ** ** * * *

 HvNAS4 GARMSFHTADVADLTDELATYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALV--ARH
 HvNAS7 GARMSFHTADVADLTDELATYDVVFLAALVGMAAEDKGQGDPHLGAHMADGAALVR-SAH
 HvNAS6 GARMSFHTADVADLTRELAAYDVVFLAALVGMAAEDKAKVIPHLGAHMADGAALVV-RSAH
 HvNAS2 GARMSFHTADVADLAGELAKYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALVVRSAH
 HvNAS3 GARMSFHTADVADLASELAKYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALVVRSAH
 HvNAS1 GARMSFHTADVADLTQELGAYDVVFLAALVGMAAEEKAKVIAHLGAHMVEGASLVV-RSA
 HvNAS5 RSRMAFHTAEVDTLTAELGAYDVVFLAALVGMTSKEKADAIAHLGKHMADGAALVREALH
 ** **** * ** ** ***** * *** ** ** **

 HvNAS4 GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVNSVIIAQSNDVHEYGLGSGR--GGR
 HvNAS7 GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVNSVIIAQSNDVHEYGLGSGR--GGR
 HvNAS6 QARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVNSVIIAHSKDVHANERPNGR--GGG
 HvNAS2 GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVNSVIIAQSNDVHADGLGSGRGAGG
 HvNAS3 GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVNSVIIAQSKEVHADGLGSARGAGR
 HvNAS1 RPRGFLYPIVDPEDIRRGGFEVLAVHHPGEVINSVIVARKEAQLSGPQNGD----A
 HvNAS5 GARAFLYPVVELDDVGRGGFQVLAVHHPAGDEVFNSFIVARKVKMSA-----
 * **** * * **** **** ** * ** * * *

 HvNAS4 YARGTVPVVSPPCRFG-EMVADVTQ--KREEFANAEEVAF
 HvNAS7 YARG-TVPVSPPCRFG-EMVADVTQ--KREEFAKAEVAF
 HvNAS6 YRGA--VPVSPPCRFG-EMVADVTQ--KREFTNAEEVAF
 HvNAS2 YARG-TVPVSPPCRFG-EMVADVTQNHKRDEFANAEEVAF
 HvNAS3 YARG-TVPVSPPCRFG-EMVADVTQNHKRDEFANAEEVAF
 HvNAS1 HARG-AVPLVSPPCNFSTKMEASALE--KSEEL TAKELAF
 ** ***** * * * * * * * * *

Fig. 8

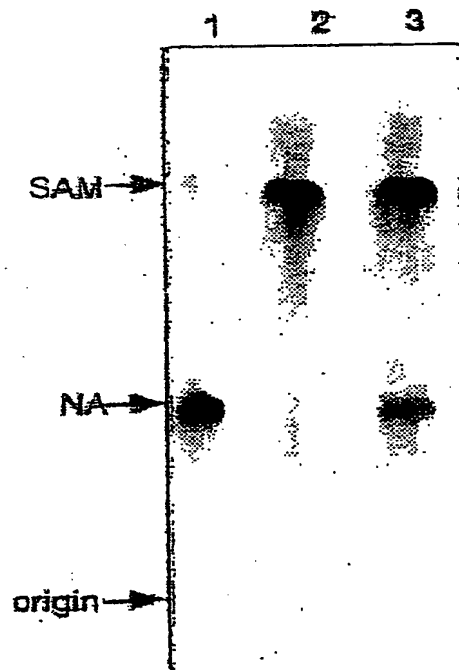
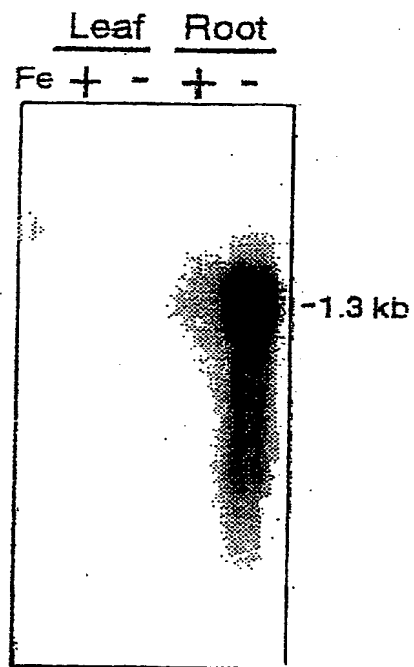


Fig. 9



T092701/ECH/950

Fig. 10

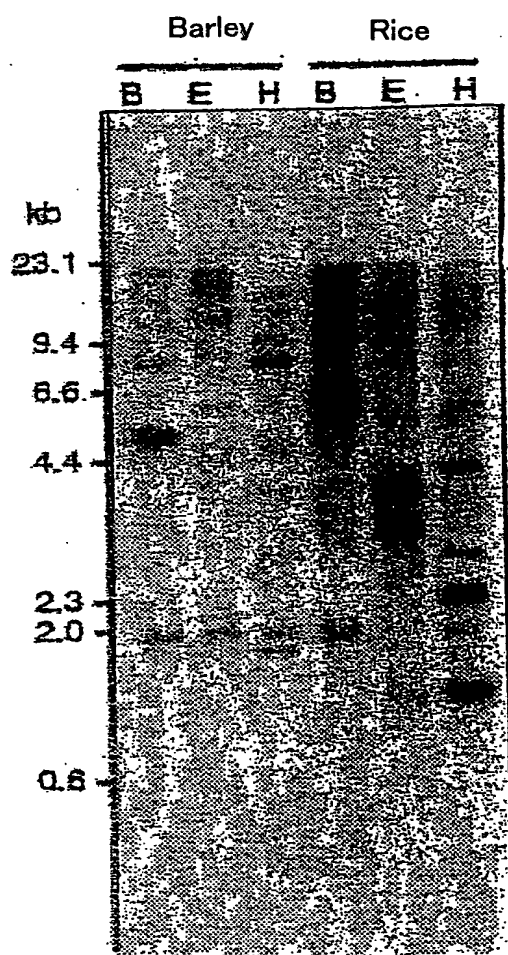


Fig. 11

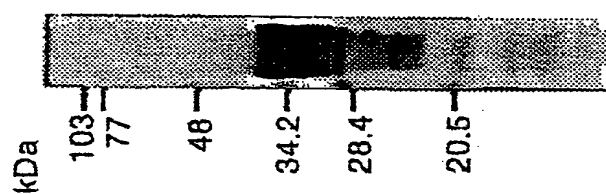


Fig. 12

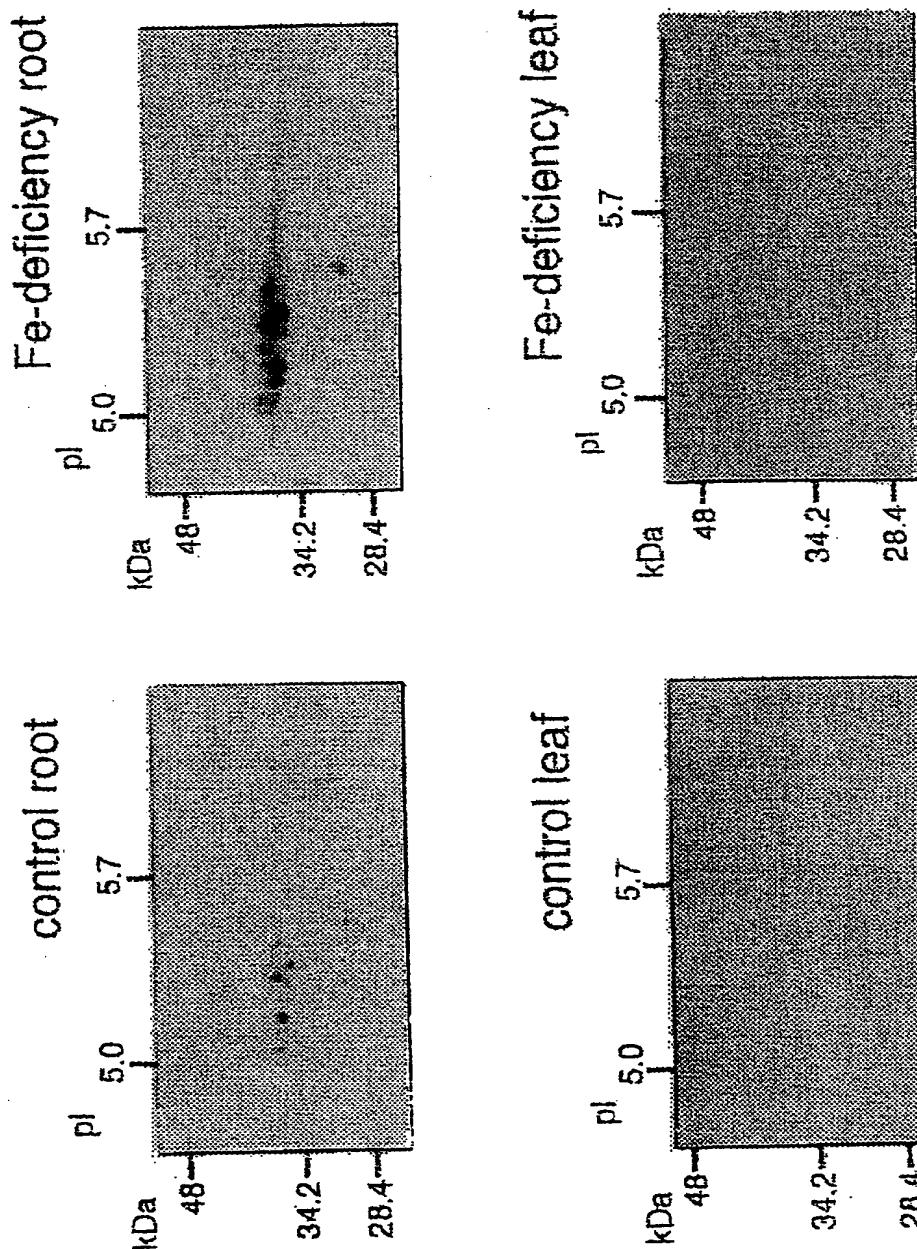


Fig. 13

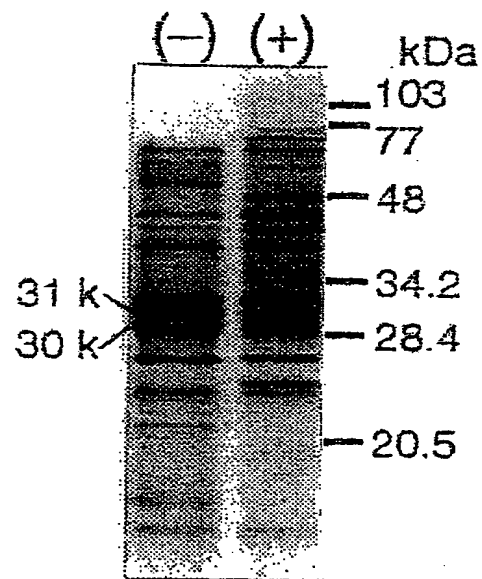


Fig. 14

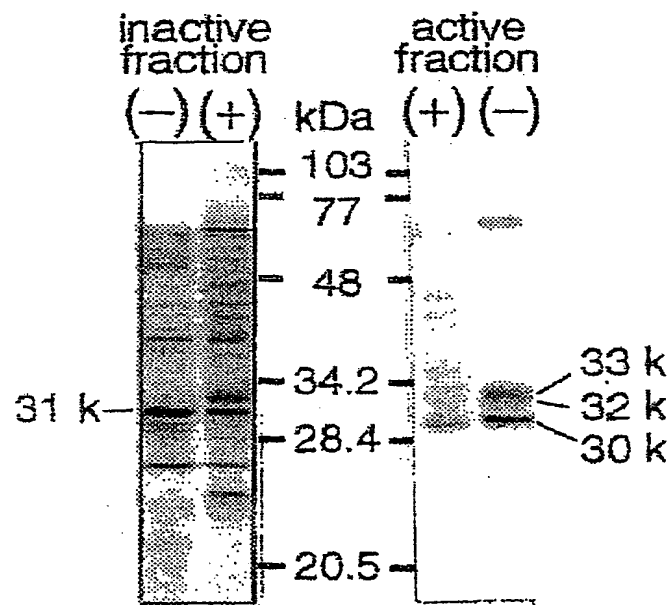


Fig. 15

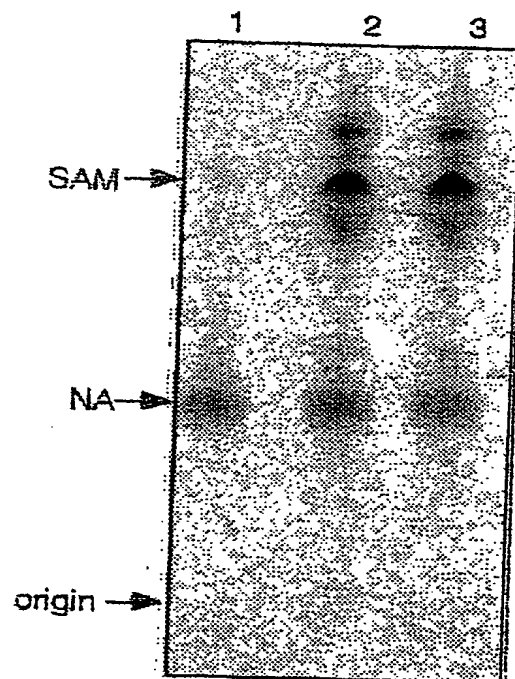


Fig. 16

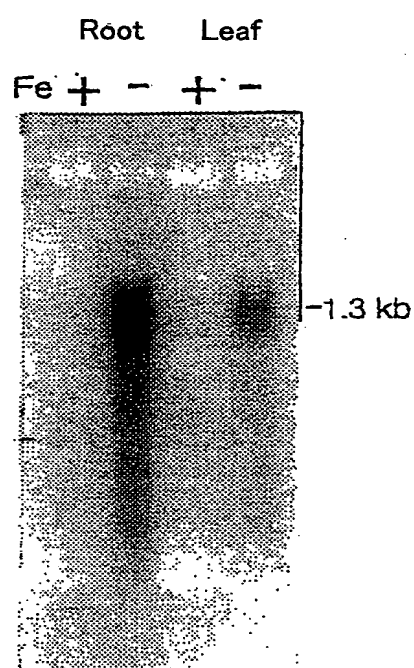


Fig. 17

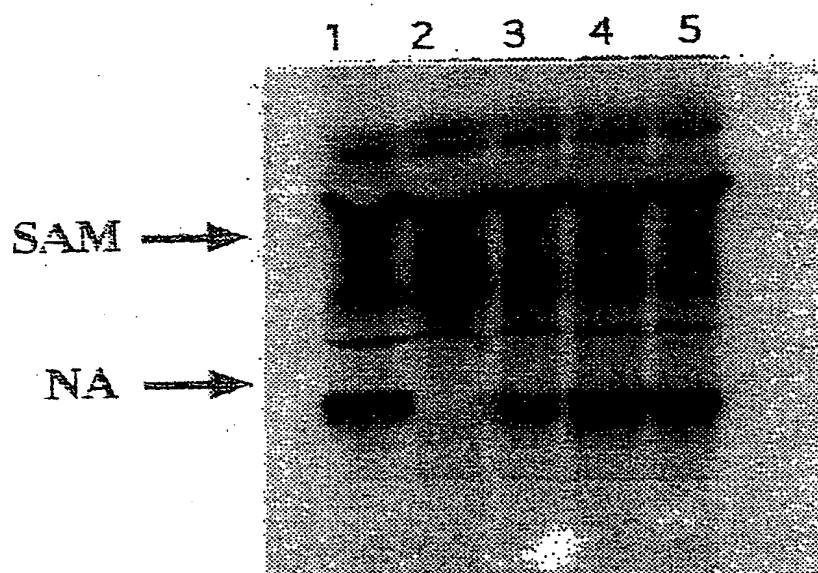


Fig. 18

